



SEQUENCE LISTING

<110> Zeneca Limited

<120> Insecticidal Proteins from Paecilomyces and Synergistic
Combinations Thereof

<130> SYN-128

<140> US 10/019,823

<141> 2001-12-21

<150> PCT/GB00/02457

<151> 2000-06-23

<150> GB 9915215.9

<151> 1999-06-29

<150> GB 9930536.9

<151> 1999-12-23

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 33

<212> PRT

<213> Paecilomyces sp.

<220>

<221> VARIANT

<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 1

Xaa	Xaa	Ile	Cys	Thr	Pro	Ala	Gly	Val	Lys	Cys	Pro	Ala	Ala	Leu	Pro
1				5					10					15	
Cys	Cys	Pro	Gly	Leu	Arg	Cys	Ile	Gly	Gly	Val	Asn	Asn	Lys	Val	Cys
			20					25					30		

Arg

<210> 2

<211> 33

<212> PRT

<213> Paecilomyces sp.

<400> 2

Gly	Lys	Ile	Cys	Thr	Pro	Ala	Gly	Val	Lys	Cys	Pro	Ala	Ala	Leu	Pro
1				5					10					15	
Cys	Cys	Pro	Gly	Leu	Arg	Cys	Ile	Gly	Gly	Val	Asn	Asn	Lys	Val	Cys
			20					25					30		

Arg

<210> 3

<211> 35

<212> PRT
<213> Paecilomyces sp.

<220>
<221> VARIANT
<222> 1, 2
<223> Xaa = Any Amino Acid

<400> 3
Xaa Xaa Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala
1 5 10 15
Leu Pro Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys
20 25 30
Val Cys Arg
35

<210> 4
<211> 332
<212> DNA
<213> Paecilomyces sp.

<400> 4
ggcaagatct gcactcctgc tggagttgta cgtatttttca tccatttcct ycaccactcc 60
tctaacatga agcaactttc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tggatctggc aagcgagacc 180
ataacatgac gcagtatact aaccctggcc gttatagaac aaggttgtga gtcgacatgt 240
tktacaacct ctacaaacgc gcgcactaat gacaacggta gtgccggtaa ttctagtgtc 300
gcaacttttg agcgtgggat aagtatgctt cg 332

<210> 5
<211> 320
<212> DNA
<213> Paecilomyces sp.

<400> 5
gggaaaatct gtacgccggc ggggggttgta cgtatttctca tccatttcct ccaccactcc 60
tctaacatga agcaactctc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180
aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300
cgtgggataa gtatgcttcg 320

<210> 6
<211> 320
<212> DNA
<213> Paecilomyces sp.

<400> 6
gggaaaatct gtacgccggc ggggggttgta cgtatttttca tccatttcct ccaccactcc 60
tctaacatga agcaactctc tcttctctct araaatgtcc cgcggctctt ccttgctgcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180
aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300
cgtgggataa gtatgcttcg 320

<210> 7
<211> 174
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide codon optimised

<400> 7

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atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcaccccg gccggcgtga agtgcccggc cgccctcccg 120
tgctgcccgg gcctccgctg catcggcggc gtgaacaaca aggtgtgccg ctga 174
```

<210> 8

<211> 174

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic polynucleotide codon optimised

<400> 8

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atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggtaaaat ttgtaccccg gccggcgtga agtgcccggc cgccctcccg 120
tggtgtccgg gcctcagggt tattggtggt gtgaataata aagtgtgtcg ctga 174
```

<210> 9

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence containing intron sequence

<400> 9

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atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcactcct gctggagttg ttgttttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa atgtcccgcg 300
gctcttcctt gctgcccccg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360
taa 363
```

<210> 10

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 10

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atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cctcctacgg caagatctgc actcctgctg gagttgtttg tttctgcttc 120
tacctttgat atatatataa taattatcat taattagtag taatataata tttcaaatat 180
ttttttcaaa ataaaagaat gtagtatata gcaattgctt ttctgtagtt tataagtgtg 240
tatattttta tttataactt ttctaataata tgaccaaacc atggtgatgt ttagaaatgt 300
cccgcggtc ttccttgctg ccccggaact cgctgcatcg gcggcgtcaa caacaagggt 360
tgccggtaa 369
```

<210> 11

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence

<400> 11

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atgggtggca gggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cctcctacat ctgcactcct gctggagttg tttgtttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatgggtg atgttttagaa atgtcccgcg 300
gctcttcctt gctgccccgg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360
taa 363
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<210> 12

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic sequence containing intron and codon
optimised

<400> 12

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atgggtggca gggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cgggcaagat ctgcaccccg gccggcgtgg tttgtttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atattttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatgggtg atgttttagaa gtgcccggcc 300
gccctcccgt gctgccccgg cctccgctgc atcggcggcg tgaacaacaa ggtgtgccgc 360
tga 363
```

<210> 13

<211> 439

<212> DNA

<213> *Paecilomyces* sp.

<400> 13

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tctacttctt catctcacgc catatatcct cccaaaatca cacctcttcc ttcaccatgc 60
aaatctccgc cgtcattgtc gcactcttcg ccagcgccgc catggccggc aagatctgca 120
ctcctgctgg agttgtacgt attttcatcc atttcctyca ccactcctct aacatgaagc 180
aactttctct tctctctaga aatgtcccgc ggctcttcct tgctgccccg gacttcgctg 240
catcggcggc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300
gtataactaac cctggccggt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360
caaacgcgcg cactaatgac aacggtagtg ccggtaattc tagtgtcgca acttttgagc 420
gtgggataag tatgcttcg 439
```

<210> 14

<211> 102

<212> DNA

<213> *Paecilomyces* sp.

<400> 14

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ggcaagatct gcactcctgc tggagttaaa tgtcccgcgg ctcttccttg ctgccccgga 60
cttcgctgca tcggcggcgt caacaacaag gtttgccggt aa 102
```

<210> 15

<211> 84

<212> DNA

<213> *Dahlia* sp.

<400> 15
 atgggttaata gatctgttgc tttttctgct tttgttctta ttctttttgt tttggctatt 60
 tcagatattg cttctgtttc agga 84

<210> 16
 <211> 87
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Radish signal sequence

<400> 16
 atggctaagt ttgcttctat tattgctctt ttgtttgctg cacttgtttt gtttgctgca 60
 tttgaagctc caactatggt tgaagct 87

<210> 17
 <211> 72
 <212> DNA
 <213> Zea mays

<400> 17
 atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
 gagatccagg cc 72

<210> 18
 <211> 90
 <212> DNA
 <213> Nicotiana sp.

<400> 18
 atgggatttg ttctcttttc acaattgcct tcatttcttc ttgtctctac acttctctta 60
 ttccctagtaa tatccactc ttgccgtgcc 90

<210> 19
 <211> 51
 <212> DNA
 <213> Paecilomyces sp.

<400> 19
 atgcaaactc ccgccgtcat tgctgcactc ttgccagcg ccgcatggc c 51

<210> 20
 <211> 28
 <212> PRT
 <213> Dahlia sp.

<400> 20
 Met Val Asn Arg Ser Val Ala Phe Ser Ala Phe Val Leu Ile Leu Phe
 1 5 10 15
 Val Leu Ala Ile Ser Asp Ile Ala Ser Val Ser Gly
 20 25

<210> 21
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Radish protein target sequence

<400> 21

```
Met Ala Lys Phe Ala Ser Ile Ile Ala Leu Leu Phe Ala Ala Leu Val
 1           5           10           15
Leu Phe Ala Ala Phe Glu Ala Pro Thr Met Val Glu Ala
          20           25
```

<210> 22

<211> 24

<212> PRT

<213> Zea Mays

<400> 22

```
Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Leu Ala Leu Val Ala Val
 1           5           10           15
Ser Leu Ala Val Glu Ile Gln Ala
          20
```

<210> 23

<211> 30

<212> PRT

<213> Nicotiana sp.

<400> 23

```
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
 1           5           10           15
Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
          20           25           30
```

<210> 24

<211> 17

<212> PRT

<213> Paecilomyces sp.

<400> 24

```
Met Gln Ile Ser Ala Val Ile Val Ala Leu Phe Ala Ser Ala Ala Met
 1           5           10           15
Ala
```

<210> 25

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 25

tcgggctcgc atgaattcgc ggccgcattt tttttttttt tttt

44

<210> 26

<211> 19

<212> DNA

<213> Artificial Sequence

<220>
 <223> Primers

 <400> 26
 tcgggctcgc atgaattcg 19

 <210> 27
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <400> 27
 atgaattcgc ggccgcat 18

 <210> 28
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <400> 28
 tcgggctcgc atgaattcgc g 21

 <210> 29
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <400> 29
 ctgcgatgaa ttcgcggccg c 21

 <210> 30
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 9, 12, 15
 <223> n = A,T,C or G

 <400> 30
 athtgyacnc cngcngg 17

 <210> 31
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

 <221> misc_feature
 <222> 9, 12, 15, 18
 <223> n = A,T,C or G

 <400> 31
 athtgyacnc cngcnggngt 20

 <210> 32
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 3, 6, 9, 12, 15
 <223> n = A,T,C or G

 <400> 32
 acnccngcng gngtnaa 17

 <210> 33
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 3, 12, 15
 <223> n = A,T,C or G

 <400> 33
 ccntgytgyc cnggnyt 17

 <210> 34
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 2, 14
 <223> n = A,T,C or G

 <400> 34
 tnaartgyat hggngg 16

 <210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

 <221> misc_feature
 <222> 3, 6, 18
 <223> n = A,T,C or G

 <400> 35
 ggngtnaaya ayaargtntg 20

 <210> 36
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 12, 15, 18, 21, 24
 <223> n = inosine

 <400> 36
 aarathtgya cncngcngg ngtnaa 26

 <210> 37
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 3, 6, 9, 12, 21, 24
 <223> n = inosine

 <400> 37
 ccngcnggng tnaartgycc ngcngc 26

 <210> 38
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 6, 9, 12, 15, 18
 <223> n = inosine

 <400> 38
 tgyccngcng cnytnccntg ytgycc 26

 <210> 39
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primers

 <221> misc_feature
 <222> 9, 12, 15
 <223> n = inosine

 <400> 39
 tgyathggng gngtnaayaa yaargt 26

 <210> 40
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <400> 40
 taaatgtccc gcggctcttc c 21

 <210> 41
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <400> 41
 cggctcttcc ttgctgcccc g 21

 <210> 42
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <400> 42
 tgctgccccg gacttcgctg c 21

 <210> 43
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primers

 <221> misc_feature
 <222> 23, 24, 25, 26, 27
 <223> n = A,T,C or G

 <400> 43
 ggtttaatta cccaagtttg agnnnnn 27

 <210> 44
 <211> 22

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primers
 <400> 44
 ctcaaacttg ggtaattaaa cc 22
 <210> 45
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primers
 <400> 45
 ggtttaatta cccaagtt 18
 <210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primers
 <400> 46
 taattaccca agtttgag 18
 <210> 47
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primers
 <400> 47
 ggtttaatta cccaagtttg ag 22
 <210> 48
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primers
 <221> misc_feature
 <222> 3, 15, 18, 21
 <223> n = inosine
 <400> 48
 canacyttrt trttnacncc ncc 23
 <210> 49
 <211> 21
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 49

atgcagcgaa gtccggggca g

21

<210> 50

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 50

ggggcagcaa ggaagagccg c

21

<210> 51

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 51

aagagccgcg ggacatttaa c

21

<210> 52

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 52

agttaaatgt cccgcggctc ttccttgctg ccccgactt cgctgcatc

49

<210> 53

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 53

gatgcagcga agtccggg

18

<210> 54

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cryIIal Embl. Accession No. X62821

<221> VARIANT

<222> 602

<223> Xaa = Any Amino Acid

<400> 54

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			20					25					30		
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr
		35					40					45			
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile
	50					55					60				
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly
65					70					75					80
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys
				85					90					95	
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile
			100					105					110		
Asn	Gln	Lys	Ile	Ser	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Thr	Asp	Leu
		115					120					125			
Lys	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Asp	Ser	Leu	Glu	Ser
	130					135					140				
Trp	Val	Gly	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Ser
145					150					155					160
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe
				165					170					175	
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala
			180					185					190		
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys
		195					200					205			
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln
	210					215					220				
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Tyr	His	Cys	Val	Lys	Trp	Tyr	Ser
225					230					235					240
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg
				245					250					255	
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val
			260					265					270		
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Gln	Met	Tyr	Pro	Ile	Lys	Thr	Thr
		275					280					285			
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His
	290					295					300				
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro
305					310					315					320
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu	Leu
				325					330					335	
Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser
			340					345					350		
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Lys	Leu	Glu	Phe	Arg
		355					360					365			
Thr	Ile	Gly	Gly	Thr	Leu	Asn	Ile	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr
	370					375					380				
Ser	Ile	Asn	Pro	Val	Thr	Leu	Pro	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg
385					390					395					400
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn
				405					410					415	
Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Val	Thr	His	Pro	Ile	Ala
			420					425					430		
Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Ala	Gly	Ile	Gly	Thr	Gln	Leu

		435					440					445					
Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Ala	Thr	Gly	Gln	Pro	Asn		
	450					455					460						
Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser	Ala		
465					470					475					480		
Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala	Asp		
			485						490					495			
Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu	Val		
		500						505					510				
Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro	Gly		
	515						520					525					
Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe	Gly		
530					535						540						
Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg	Val		
545				550					555						560		
Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser	Ile		
			565					570					575				
Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn	Arg		
		580					585						590				
Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Xaa	Thr	Val	Gly	Phe	Thr	Thr		
	595					600						605					
Pro	Phe	Ser	Leu	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala	Trp		
610					615						620						
Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe	Val		
625				630						635					640		
Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala	Gln		
			645					650						655			
Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu	Lys		
		660					665						670				
Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	Glu		
	675					680						685					
Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe	Glu		
690					695					700							
Ile	Val	Lys	Tyr	Ala	Lys	Gln	Leu	His	Ile	Glu	Arg	Asn	Met				
705					710					715							

<210> 55

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cryIIa2 Embl. Accession No. M98544

<400> 55

Met	Lys	Leu	Lys	Asn	Gln	Asp	Lys	His	Gln	Ser	Phe	Ser	Ser	Asn	Ala		
1				5					10					15			
Lys	Val	Asp	Lys	Ile	Ser	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile		
			20				25						30				
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr		
	35				40						45						
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile		
	50				55						60						
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly		
65				70					75						80		
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys		
			85				90						95				
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile		
		100					105						110				

Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Val	Gly	Phe	Thr
		595					600					605			
Thr	Pro	Phe	Ser	Phe	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
	610					615					620				
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
	625				630					635					640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala
				645					650					655	
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu
			660					665					670		
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val
		675					680					685			
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe
	690					695					700				
Glu	Ile	Val	Lys	Tyr	Ala	Lys	Gln	Leu	His	Ile	Glu	Arg	Asn	Met	
705					710					715					

<210> 56

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia3 Embl. Accession No. L36338

<400> 56

Met	Lys	Leu	Lys	Asn	Gln	Asp	Lys	His	Gln	Ser	Phe	Ser	Ser	Asn	Ala
1				5					10					15	
Lys	Val	Asp	Lys	Ile	Ser	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile
			20					25					30		
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr
		35					40					45			
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile
	50					55					60				
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly
65				70					75						80
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys
				85					90					95	
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Phe	Met	Glu	His	Val	Glu	Glu	Ile	Ile
			100					105					110		
Asn	Gln	Lys	Ile	Ser	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Thr	Asp	Leu
		115					120					125			
Lys	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Asp	Ser	Leu	Glu	Ser
	130					135					140				
Trp	Val	Gly	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Ser
145					150					155					160
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe
				165					170					175	
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala
			180					185					190		
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys
		195					200					205			
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln
	210					215					220				
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Tyr	His	Cys	Val	Lys	Trp	Tyr	Ser
225					230					235					240
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg
				245					250					255	
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val

			260					265				270			
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Gln	Met	Tyr	Pro	Ile	Lys	Thr	Thr
		275					280					285			
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His
	290					295					300				
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro
305					310					315					320
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu	Leu
				325					330					335	
Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser
			340					345					350		
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Lys	Leu	Glu	Phe	Arg
		355					360					365			
Thr	Ile	Gly	Gly	Thr	Leu	Asn	Ile	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr
	370					375					380				
Ser	Ile	Asn	Pro	Val	Thr	Leu	Pro	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg
385					390					395					400
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn
				405					410					415	
Gly	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Val	Thr	His	Pro	Ile
			420					425					430		
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Ala	Gly	Ile	Gly	Thr	Gln
		435					440					445			
Leu	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Ala	Thr	Gly	Gln	Pro
	450					455					460				
Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser
465					470					475					480
Ala	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala
				485					490					495	
Asp	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu
			500					505					510		
Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro
		515					520					525			
Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe
	530					535					540				
Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg
545					550					555					560
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser
				565					570					575	
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn
			580					585					590		
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Val	Gly	Phe	Thr
		595					600					605			
Thr	Pro	Phe	Ser	Phe	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
	610					615					620				
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
625					630					635					640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala
				645					650					655	
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu
			660					665					670		
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val
		675					680					685			
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe
	690					695					700				
Glu	Ile	Val	Lys	Tyr	Ala	Asn	Glu	Leu	His	Ile	Glu	Arg	Asn	Met	
705					710					715					

<210> 57

<211> 719
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PROTEIN cryIIa4 Embl. Accession No. L49391

<400> 57
 Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1 5 10 15
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35 40 45
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95
 Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
 100 105 110
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
 115 120 125
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
 130 135 140
 Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
 165 170 175
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
 180 185 190
 Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
 195 200 205
 Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
 210 215 220
 Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
 225 230 235 240
 Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
 245 250 255
 Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
 260 265 270
 Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
 275 280 285
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
 290 295 300
 Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
 305 310 315 320
 Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
 325 330 335
 Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
 340 345 350
 Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
 355 360 365
 Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
 370 375 380
 Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
 385 390 395 400
 Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
 405 410 415

Gly	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Val	Thr	His	Pro	Ile
			420					425					430		
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Val	Gly	Ile	Gly	Thr	Gln
		435					440					445			
Leu	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Ala	Thr	Gly	Gln	Pro
	450					455					460				
Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser
465					470					475					480
Ala	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala
				485					490					495	
Asp	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu
			500					505					510		
Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro
		515					520					525			
Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe
	530					535					540				
Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg
545					550					555					560
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser
				565					570					575	
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn
			580					585					590		
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Val	Gly	Phe	Thr
		595					600					605			
Thr	Pro	Phe	Ser	Phe	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala
	610					615						620			
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe
625					630					635					640
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala
				645					650					655	
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu
			660					665					670		
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val
		675					680					685			
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe
	690					695					700				
Glu	Ile	Val	Lys	Tyr	Ala	Lys	Gln	Leu	His	Ile	Glu	Arg	Asn	Met	
705					710					715					

<210> 58

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ia5 Embl. Accession No. Y08920

<400> 58

Met	Lys	Leu	Lys	Asn	Gln	Asp	Lys	His	Gln	Ser	Phe	Ser	Ser	Asn	Ala
1				5					10					15	
Lys	Val	Asp	Lys	Ile	Ser	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile
			20					25					30		
Glu	Leu	Gln	Asn	Ile	Asn	His	Glu	Asp	Cys	Leu	Lys	Met	Ser	Glu	Tyr
		35					40					45			
Glu	Asn	Val	Glu	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile
	50					55					60				
Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly
65					70					75					80
Gln	Val	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys

				85				90					95			
Gly	Lys	Asn	Gln	Trp	Glu	Ile	Leu	Phe	Met	Glu	His	Val	Glu	Glu	Ile	
			100					105					110			
Asn	Gln	Lys	Ile	Ser	Thr	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Thr	Asp	Leu	
		115					120					125				
Lys	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Asp	Ser	Leu	Glu	Ser	
	130					135					140					
Trp	Val	Gly	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Arg	Ser	
145					150					155					160	
Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe	
				165				170						175		
Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala	
			180					185					190			
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Lys	
		195					200					205				
Glu	Trp	Gly	Leu	Ser	Ser	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln	
	210					215					220					
Val	Glu	Arg	Ala	Gly	Asp	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Ser	
225					230					235					240	
Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Val	Arg	
				245					250					255		
Tyr	Asn	Gln	Phe	Arg	Arg	Asp	Met	Thr	Leu	Met	Val	Leu	Asp	Leu	Val	
			260					265					270			
Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Gln	Met	Tyr	Pro	Ile	Lys	Thr	Thr	
		275					280					285				
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His	
	290					295					300					
Pro	His	Pro	Ser	Phe	Thr	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro	
305					310					315					320	
Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Val	Arg	Asn	Pro	His	Leu	Leu	
				325					330					335		
Asp	Phe	Leu	Glu	Gln	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser	
			340					345					350			
Asn	Thr	Gln	Tyr	Met	Asn	Met	Trp	Gly	Gly	His	Lys	Leu	Glu	Phe	Arg	
		355					360					365				
Thr	Ile	Gly	Gly	Thr	Leu	Asn	Ile	Ser	Thr	Gln	Gly	Ser	Thr	Asn	Thr	
	370					375					380					
Ser	Ile	Asn	Pro	Val	Thr	Leu	Pro	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg	
385					390					395					400	
Thr	Glu	Ser	Leu	Ala	Gly	Leu	Asn	Leu	Phe	Leu	Thr	Gln	Pro	Val	Asn	
				405					410					415		
Gly	Val	Pro	Arg	Val	Asp	Phe	His	Trp	Lys	Phe	Val	Thr	His	Pro	Ile	
			420					425					430			
Ala	Ser	Asp	Asn	Phe	Tyr	Tyr	Pro	Gly	Tyr	Ala	Gly	Ile	Gly	Thr	Gln	
		435					440					445				
Leu	Gln	Asp	Ser	Glu	Asn	Glu	Leu	Pro	Pro	Glu	Ala	Thr	Gly	Gln	Pro	
	450					455				460						
Asn	Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ser	
465					470					475					480	
Ala	Ser	His	Val	Lys	Ala	Leu	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala	
				485					490					495		
Asp	Arg	Thr	Asn	Thr	Ile	Glu	Pro	Asn	Ser	Ile	Thr	Gln	Ile	Pro	Leu	
			500					505				510				
Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro	
		515					520					525				
Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe	
	530					535					540					
Gly	Asp	Ile	Arg	Val	Asn	Ile	Asn	Pro	Pro	Phe	Ala	Gln	Arg	Tyr	Arg	
545					550					555					560	
Val	Arg	Ile	Arg	Tyr	Ala	Ser	Thr	Thr	Asp	Leu	Gln	Phe	His	Thr	Ser	

				565					570					575			
Ile	Asn	Gly	Lys	Ala	Ile	Asn	Gln	Gly	Asn	Phe	Ser	Ala	Thr	Met	Asn		
			580					585					590				
Arg	Gly	Glu	Asp	Leu	Asp	Tyr	Lys	Thr	Phe	Arg	Thr	Val	Gly	Phe	Thr		
		595					600					605					
Thr	Pro	Phe	Ser	Phe	Leu	Asp	Val	Gln	Ser	Thr	Phe	Thr	Ile	Gly	Ala		
	610					615					620						
Trp	Asn	Phe	Ser	Ser	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Ile	Glu	Phe		
625					630					635					640		
Val	Pro	Val	Glu	Val	Thr	Tyr	Glu	Ala	Glu	Tyr	Asp	Phe	Glu	Lys	Ala		
				645					650					655			
Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu		
			660					665					670				
Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val		
		675					680					685					
Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe		
	690					695					700						
Glu	Ile	Val	Lys	Tyr	Ala	Asn	Glu	Leu	His	Ile	Glu	Arg	Asn	Met			
705					710					715							

<210> 59

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cryIb1 Embl. Accession No. U07642

<400> 59

Met	Lys	Leu	Lys	Asn	Pro	Asp	Lys	His	Gln	Ser	Leu	Ser	Ser	Asn	Ala		
1				5					10					15			
Lys	Val	Asp	Lys	Ile	Ala	Thr	Asp	Ser	Leu	Lys	Asn	Glu	Thr	Asp	Ile		
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Glu	Ser	Ile	Asp	Pro	Phe	Val	Ser	Ala	Ser	Thr	Ile	Gln	Thr	Gly	Ile		
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Gly	Ile	Ala	Gly	Lys	Ile	Leu	Gly	Thr	Leu	Gly	Val	Pro	Phe	Ala	Gly		
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Gln	Ile	Ala	Ser	Leu	Tyr	Ser	Phe	Ile	Leu	Gly	Glu	Leu	Trp	Pro	Lys		
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			100					105					110				
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Arg	Gly	Leu	Gly	Asp	Ala	Leu	Ala	Val	Tyr	His	Glu	Ser	Leu	Glu	Ser		
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Trp	Val	Glu	Asn	Arg	Asn	Asn	Thr	Arg	Ala	Arg	Ser	Val	Val	Lys	Asn		
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Gln	Tyr	Ile	Ala	Leu	Glu	Leu	Met	Phe	Val	Gln	Lys	Leu	Pro	Ser	Phe		
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Ala	Val	Ser	Gly	Glu	Glu	Val	Pro	Leu	Leu	Pro	Ile	Tyr	Ala	Gln	Ala		
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Glu	Trp	Gly	Leu	Ser	Ala	Ser	Glu	Ile	Ser	Thr	Phe	Tyr	Asn	Arg	Gln		
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Val	Glu	Arg	Thr	Arg	Asp	Tyr	Ser	Asp	His	Cys	Ile	Lys	Trp	Tyr	Asn		
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Thr	Gly	Leu	Asn	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Lys	Ser	Trp	Val	Arg	
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Ala	Leu	Phe	Pro	Ser	Tyr	Asp	Thr	Leu	Val	Tyr	Pro	Ile	Lys	Thr	Thr	
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Ser	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Ala	Ile	Gly	Thr	Val	His	
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Pro	Asn	Gln	Ala	Phe	Ala	Ser	Thr	Thr	Trp	Tyr	Asn	Asn	Asn	Ala	Pro	
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Ser	Phe	Ser	Ala	Ile	Glu	Ala	Ala	Val	Ile	Arg	Ser	Pro	His	Leu	Leu	
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Asp	Phe	Leu	Glu	Lys	Val	Thr	Ile	Tyr	Ser	Leu	Leu	Ser	Arg	Trp	Ser	
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Val	Lys	Ala	Phe	Asn	Leu	Ser	Ser	Gly	Ala	Ala	Val	Val	Arg	Gly	Pro	
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	530					535					540					
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Gln	Glu	Lys	Val	Thr	Ala	Leu	Phe	Thr	Ser	Thr	Asn	Pro	Arg	Gly	Leu	
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Lys	Thr	Asp	Val	Lys	Asp	Tyr	His	Ile	Asp	Gln	Val	Ser	Asn	Leu	Val	
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Glu	Ser	Leu	Ser	Asp	Glu	Phe	Tyr	Leu	Asp	Glu	Lys	Arg	Glu	Leu	Phe	
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 Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 20 25 30
 Xaa

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 <213> Paecilomyces sp.

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 ctctgtctgg agttgtacgt attttcatcc atttcctyca ccactcctct aacatgaagc 180
 aactttctct tctctctaga aatgtccgcg ggctcttcct tgctgccccg gacttcgctg 240
 catcgccggc gtcaacgtaa gtcacatgg atctggcaag cgagaccata acatgacgca 300
 gtatactaac cctggccggt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360
 caaacgcgcg cactaatgac aacggtagtg ccggtaattc tagtgctgca acttttgagc 420
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 cgccgctcatt gtcgcactct tcgccagcgc cgccatggcc ggcaagatct gcactcctgc 180
 tggagttaaa tgtcccgcggt ctcttccttg ctgccccgga ctctgctgca tcggcggcgt 240
 caacaacaag gtttgccggt aattctagtg tcgcaacttt tgagcgtggg ataagtatgc 300
 ttcgttcggt gtatggagtt ctctccgga gtttaagctc ggccggtcga cagcgggtct 360
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<211> 5

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